

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David White et al.  
Serial No.: 09/195,896  
Filed : November 19, 1998  
Title : LEPTIN INDUCED GENES

Art Unit:  
Examiner:

Box Sequence  
Assistant Commissioner for Patents  
Washington, DC 20231

VERIFIED STATEMENT UNDER 37 CFR § 1.821 (f)

I, Maureen Ruttle, declare that I personally prepared the paper and the computer-readable copies of the Sequence Listing filed herewith in the above-entitled case and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: Nov 15, 1999

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Date of Deposit November 29, 1999  
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as **first class mail** with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Carrie A. Amonte

## SEQUENCE LISTING

<110> White, David  
Zhou, Jianghong  
Tartaglia, Louis A.

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<140> US 09/195,896

<141> 1998-11-19

<150> US 60/108,379

<151> 1998-10-29

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Leu 50	Pro	Gly	Arg	Ala	Gly	Phe 55	Lys	Glu	Asn	Pro	Val 60	Thr	Tyr	Thr	Phe
Arg 65	Gly	Phe	Arg	Ser	Thr 70	Lys	Ser	Glu	Thr 75	Asn	His	Ser	Ser	Leu	Arg 80
Asn	Ile	Trp	Lys 85	Glu	Thr	Val	Pro	Gln 90	Thr	Leu	Arg	Pro	Gln 95	Thr	Ala
Thr	Asn	Ser	Asn 100	Asn	Thr	Asp	Leu	Ser 105	Pro	Gln	Gly	Val 110	Thr	Gly	Leu
Glu	Asn	Thr 115	Leu	Ser	Ala	Asn	Gly 120	Ser	Ile	Tyr	Asn	Glu 125	Lys	Gly	Thr
Gly	His 130	Pro	Asn	Ser	Tyr	His 135	Phe	Lys	Tyr	Ile	Ile 140	Asn	Glu	Pro	Glu
Lys 145	Cys	Gln	Glu	Lys	Ser 150	Pro	Phe	Leu	Ile	Leu 155	Leu	Ile	Ala	Ala	Glu 160
Pro	Gly	Gln	Ile 165	Glu	Ala	Arg	Arg	Ala 170	Ile	Arg	Gln	Thr	Trp	Gly 175	Asn
Glu	Ser	Leu 180	Ala	Pro	Gly	Ile	Gln 185	Ile	Thr	Arg	Ile	Phe 190	Leu	Leu	Gly
Leu	Ser	Ile 195	Lys	Leu	Asn	Gly	Tyr 200	Leu	Gln	Arg	Ala	Ile 205	Leu	Glu	Glu
Ser	Arg 210	Gln	Tyr	His	Asp	Ile 215	Ile	Gln	Gln	Glu	Tyr 220	Leu	Asp	Thr	Tyr
Tyr 225	Asn	Leu	Thr	Ile	Lys 230	Thr	Leu	Met	Gly	Met 235	Asn	Trp	Val	Ala	Thr 240
Tyr	Cys	Pro	His 245	Ile	Pro	Tyr	Val	Met	Lys 250	Thr	Asp	Ser	Asp	Met 255	Phe
Val	Asn	Thr 260	Glu	Tyr	Leu	Ile	Asn 265	Lys	Leu	Leu	Lys	Pro	Asp 270	Leu	Pro
Pro	Arg 275	His	Asn	Tyr	Phe	Thr	Gly 280	Tyr	Leu	Met	Arg	Gly 285	Tyr	Ala	Pro
Asn	Arg 290	Asn	Lys	Asp	Ser	Lys 295	Trp	Tyr	Met	Pro	Pro 300	Asp	Leu	Tyr	Pro

Ser Glu Arg Tyr Pro Val Phe Cys Ser Gly Thr Gly Tyr Val Phe Ser  
 305 310 315 320  
 Gly Asp Leu Ala Glu Lys Ile Phe Lys Val Ser Leu Gly Ile Arg Arg  
 325 330 335  
 Leu His Leu Glu Asp Val Tyr Val Gly Ile Cys Leu Ala Lys Leu Arg  
 340 345 350  
 Ile Asp Pro Val Pro Pro Pro Asn Glu Phe Val Phe Asn His Trp Arg  
 355 360 365  
 Val Ser Tyr Ser Ser Cys Lys Tyr Ser His Leu Ile Thr Ser His Gln  
 370 375 380  
 Phe Gln Pro Ser Glu Leu Ile Lys Tyr Trp Asn His Leu Gln Gln Asn  
 385 390 395 400  
 Lys His Asn Ala Cys Ala Asn Ala Ala Lys Glu Lys Ala Gly Arg Tyr  
 405 410 415  
 Arg His Arg Lys Leu His  
 420

<210> 12  
 <211> 229  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> VARIANT  
 <222> (1)...(229)  
 <223> Xaa = Any Amino Acid

<400> 12  
 Met Ala Xaa Arg Arg Lys Val Leu Leu Arg Leu Leu Val Leu Ser Leu  
 1 5 10 15  
 Val Xaa Leu Xaa Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Phe Pro  
 20 25 30  
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser  
 35 40 45  
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn  
 50 55 60  
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe  
 65 70 75 80  
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu  
 85 90 95  
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala  
 100 105 110  
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val  
 115 120 125  
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa  
 130 135 140  
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile  
 145 150 155 160  
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu  
 165 170 175  
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val  
 180 185 190  
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn  
 195 200 205  
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly  
 210 215 220  
 Tyr Val Ile Xaa Gly  
 225

<210> 13  
 <211> 1707  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (246)...(1436)

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1707)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 13

acgcgtccgc gcagcggcag cggcagcagc ggcaacaagt gccggaggct agcagagcca	60
agccggagca gtccctgccg ccgacaccgc cgggccgccc gtccggggcg ccgcgcatgg	120
agcgtgagct gcggcggtcg ccgggctgag ccgcgcggag cggccgggac gtggatgtgg	180
ccgcgatctc ccgcccttgc ccccgccccg ccgagctgga gctgctcccg gacaagatat	240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg	290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met	
1 5 10 15	
atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt	338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser	
20 25 30	
agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag	386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys	
35 40 45	
ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa	434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln	
50 55 60	
gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac	482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn	
65 70 75	
cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac	530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr	
80 85 90 95	
tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac	578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn	
100 105 110	
ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat	626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn	
115 120 125	
tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc	674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe	
130 135 140	
ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa	722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln	
145 150 155	
gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg	770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr	
160 165 170 175	
gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac	818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His	
180 185 190	

ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac 866  
 Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp  
 195 200 205  
 att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag 914  
 Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys  
 210 215 220  
 gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag 962  
 Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu  
 225 230 235  
 ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc 1010  
 Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile  
 240 245 250 255  
 ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc 1058  
 Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe  
 260 265 270  
 ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg 1106  
 Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu  
 275 280 285  
 aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat 1154  
 Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr  
 290 295 300  
 gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg 1202  
 Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu  
 305 310 315  
 tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat 1250  
 Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr  
 320 325 330 335  
 act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa 1298  
 Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys  
 340 345 350  
 ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc 1346  
 Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys  
 355 360 365  
 tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg 1394  
 Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met  
 370 375 380  
 att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc 1436  
 Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
 385 390 395  
 taaaatagat acaaaactcaa tttkgsatwg raaggggtwt tttgratwgg ycccatgttg 1496  
 ggggtctcaca ttagagtaat ttctatttna ancatgaaat tgcctttatg agtgataccc 1556  
 atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta 1616  
 atttntttat ggtgaatggc aggatattgg tctgacttac cgntagggga ntttaaaact 1676  
 ggnoccttttt gaatctgttt ggatggccct t 1707

&lt;210&gt; 14

&lt;211&gt; 397

<212> PRT  
<213> Homo sapiens

<400> 14  
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met  
1 5 10 15  
Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser  
20 25 30  
Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe  
35 40 45  
Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu  
50 55 60  
Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln  
65 70 75 80  
Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys  
85 90 95  
Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu  
100 105 110  
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
115 120 125  
Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu  
130 135 140  
Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala  
145 150 155 160  
Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val  
165 170 175  
Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro  
180 185 190  
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile  
195 200 205  
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
210 215 220  
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe  
225 230 235 240  
Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
245 250 255  
Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile  
260 265 270  
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
275 280 285  
Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala  
290 295 300  
Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr  
305 310 315 320  
His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
325 330 335  
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
340 345 350  
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser  
355 360 365  
Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
370 375 380  
Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
385 390 395

<210> 15  
<211> 365  
<212> PRT  
<213> Homo sapiens

<400> 15  
 Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe  
 1 5 10 15  
 Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu  
 20 25 30  
 Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln  
 35 40 45  
 Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys  
 50 55 60  
 Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu  
 65 70 75 80  
 Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr  
 85 90 95  
 Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu  
 100 105 110  
 Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Gln Ala  
 115 120 125  
 Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val  
 130 135 140  
 Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro  
 145 150 155 160  
 Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile  
 165 170 175  
 Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu  
 180 185 190  
 Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe  
 195 200 205  
 Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu  
 210 215 220  
 Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile  
 225 230 235 240  
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys  
 245 250 255  
 Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala  
 260 265 270  
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr  
 275 280 285  
 His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr  
 290 295 300  
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly  
 305 310 315 320  
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser  
 325 330 335  
 Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile  
 340 345 350  
 Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys  
 355 360 365

<210> 16

<211> 20

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> (1)...(20)

<223> Synthetically generated primer

<400> 16

cttcgacgcc ccacactcat

<210> 17  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Artificial sequence  
<222> (1)...(20)  
<223> Synthetically generated primer

<400> 17  
atgagtgtgg ggcgtcgaag